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<110> Daniel Cohen
       Ilya Chumakov

<120> Treatment of CNS Disorders Using D-Amino Acid Oxidase and D-Aspartate
       Oxidase Antagonists

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18

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ctg gag gga aag aac tat cta cag tgg ctg act gaa agg tta act gag      605
Leu Glu Gly Lys Asn Tyr Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu
              140                145                150
agg gga gtg aag ttc ttc cag cgg aaa gtg gag tct ttt gag gag gtg      653
Arg Gly Val Lys Phe Phe Gln Arg Lys Val Glu Ser Phe Glu Glu Val
155                160                165                170
gca aga gaa ggc gca gac gtg att gtc aac tgc act ggg gta tgg gct      701
Ala Arg Glu Gly Ala Asp Val Ile Val Asn Cys Thr Gly Val Trp Ala
              175                180                185
ggg gcg cta caa cga gac ccc ctg ctg cag cca ggc cgg ggg cag atc      749
Gly Ala Leu Gln Arg Asp Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile
              190                195                200
atg aag gtg gac gcc cct tgg atg aag cac ttc att ctc acc cat gac      797
Met Lys Val Asp Ala Pro Trp Met Lys His Phe Ile Leu Thr His Asp
              205                210                215
cca gag aga ggc atc tac aat tcc ccg tac atc atc cca ggg acc cag      845
Pro Glu Arg Gly Ile Tyr Asn Ser Pro Tyr Ile Ile Pro Gly Thr Gln
              220                225                230
aca gtt act ctt gga ggc atc ttc cag ttg gga aac tgg agt gaa cta      893
Thr Val Thr Leu Gly Gly Ile Phe Gln Leu Gly Asn Trp Ser Glu Leu
235                240                245                250
aac aat atc cag gac cac aac acc att tgg gaa ggc tgc tgc aga ctg      941
Asn Asn Ile Gln Asp His Asn Thr Ile Trp Glu Gly Cys Cys Arg Leu
              255                260                265
gag ccc aca ctg aag aat gca aga att att ggt gaa cga act ggc ttc      989
Glu Pro Thr Leu Lys Asn Ala Arg Ile Ile Gly Glu Arg Thr Gly Phe
              270                275                280
cgg cca gta cgc ccc cag att cgg cta gaa aga gaa cag ctt cgc act     1037
Arg Pro Val Arg Pro Gln Ile Arg Leu Glu Arg Glu Gln Leu Arg Thr
              285                290                295
gga cct tca aac aca gag gtc atc cac aac tat ggc cat gga ggc tac     1085
Gly Pro Ser Asn Thr Glu Val Ile His Asn Tyr Gly His Gly Gly Tyr
              300                305                310
ggg ctc acc atc cac tgg gga tgt gcc ctg gag gca gcc aag ctc ttt     1133
Gly Leu Thr Ile His Trp Gly Cys Ala Leu Glu Ala Ala Lys Leu Phe
315                320                325                330
ggg aga atc ctg gaa gaa aag aaa ttg tcc aga atg cca cca tcc cac     1181
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32

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          Gly Arg Ile Leu Glu Glu Lys Lys Leu Ser Arg Met Pro Pro Ser His
                  335                 340                 345
          ctc tgaagactcc agtgactgct gcctcccccc acaagaactc ccttctcccc        1234
          Leu
          tcagccaatg aatcaatgtg ctccttcata agccattgct tctccctcac ttctttcctc   1294
          aaagaagcat gaggtgagag aaagccacaa agtcagtgcc tggagaaggg ttcagcccaa   1354
          catggggccc ctctcatcac tgaaatccct ctaccttctc tgggtctggc attataaaga   1414
          acagctgagg ctgtcattcc atgagtcttc agaagaaagg acagctcaga aaatcaaaga   1474
          ggccaactgc ccagagccac agaaaatgga ggataattga ggctaagtaa cctgattaca   1534
          agttgtacta acatattaaa ggttctgaaa agtcctgcag caaagacaac tatctgatgt   1594
          tgtttaaccc agtgcttgct aaacctatct ggctatggaa ctcttttgcc cagagcaccc   1654
          atgaatgcca tgacacaaat ctgagaaaat gctggaa                           1691


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          tcctccatgt tattcacagg gtctcagcac gattcatctc aaagcagcga aacaagcact   120
          ggcctcagaa gaagcaatat taaaacagtt acaactcatc tagcgcacag acacccaact   180
          gacaccctgt tcctccagtc ataacaacaa ctacagcttt gattgaacaa gagactgagt   240
          ttggtaactt tctcctaata aaaagatcac tgactatgga ctgcttctgg tggggttacg   300
          aaaccgcaac ctcatgtgcc tgcatttcct gaaaagacat tttgatgtag aagggcctg    360
          gagtcctgct gcttgcgtct ctgggatacg ggagcaaaga gccacgcatc ctcatggccc   420
          acacaggcgt cacctccagt ctctccttgg cctcatctcc ccagcgtcct ggaatggcat   480
          cgggctggcc caggagccc ctgtcctgtg cctctccttt ccctcaggg gctgccaggc   540
          tgaccacccc caccgcaggc caggcctaca gtgcccatg gaacgtcctg accctccccc   600
          agggtggcag caggaagaag gaagaaaggg gatcctctcc agctggccag agagacagac   650
          cttcttgtgc tcatcaaccc tccaagaatg cctgccctcc ctccttcccc caaggcctgt   720
          ccacaggggc ttgagatcag ccagaaaagt caggcaactt ttcagggact gggagcgagg   780
          tctcccggcc gggcctgggt ccagtctctg tgggcagtgc agtgccgagc cccacccctc   840
          aagccgtgcc ctgtccatag ctccagactt tgacctgca ctccagtccg ggctggcgga   900
          cagagggctg gaaacaagac gctccagaat caggagcttc ccctcaggaa atagcatcct   960
          gtgtccccgc actgcagttg tctggtctct ccagcagttt ggtacttccg atgaagagct   1020
          tgtgtctcca gaggcaaagt atgggggaag agggaagaga gaagaccaag ggtccctgag   1080
          aggggctgtc ccctaagccc cagtatccaa gctcgggctc gaagctggaa ggagaattgc   1140
          ctagaggctg ctgca atg cgt gtg gtg gtg att gga gca gga gtc atc ggg   1191
                           Met Arg Val Val Val Ile Gly Ala Gly Val Ile Gly
                            1               5                  10
          ctg tcc acc gcc ctc tgc atc cat gag cgc tac cac tca gtc ctg cag   1239
          Leu Ser Thr Ala Leu Cys Ile His Glu Arg Tyr His Ser Val Leu Gln
              15                  20                  25
          cca ctg gac ata aag gtc tac gcg gac cgc ttc acc cca ctc acc acc   1287
          Pro Leu Asp Ile Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr
              30                  35                  40
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33

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acc gac gtg gct gcc ggc ctc tgg cag ccc tac ctt tct gac ccc aac      1335
Thr Asp Val Ala Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn
45               50                  55                  60
aac cca cag gag gcg gac tgg agc caa cag acc ttt gac tat ctc ctg      1383
Asn Pro Gln Glu Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu
                65                  70                  75
agc cat gtc cat tct ccc aac gct gaa aac ctg ggc ctg ttc cta atc      1431
Ser His Val His Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile
            80                  85                  90
tcg ggc tac aac ctc ttc cat gaa gcc att ccg gac cct tcc tgg aag      1479
Ser Gly Tyr Asn Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp Lys
            95                  100                 105
gac aca gtt ctg gga ttt cgg aag ctg acc ccc aga gag ctg gat atg      1527
Asp Thr Val Leu Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp Met
    110                 115                 120
ttc cca gat tac ggc tat ggc tgg ttc cac aca agc cta att ctg gag      1575
Phe Pro Asp Tyr Gly Tyr Gly Trp Phe His Thr Ser Leu Ile Leu Glu
125                 130                 135                 140
gga aag aac tat cta cag tgg ctg act gaa agg tta act gag agg gga      1623
Gly Lys Asn Tyr Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg Gly
                145                 150                 155
gtg aag ttc ttc cag cgg aaa gtg gag tct ttt gag gag gtg gca aga      1671
Val Lys Phe Phe Gln Arg Lys Val Glu Ser Phe Glu Glu Val Ala Arg
                160                 165                 170
gaa ggc gca gac gtg att gtc aac tgc act ggg gta tgg gct ggg gcg      1719
Glu Gly Ala Asp Val Ile Val Asn Cys Thr Gly Val Trp Ala Gly Ala
            175                 180                 185
cta caa cga gac ccc ctg ctg cag cca ggc cgg ggg cag atc atg aag      1767
Leu Gln Arg Asp Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile Met Lys
            190                 195                 200
gac cca gac agt tac tct tgg agg cat ctt cca gtt ggg aaa ctg gag      1815
Asp Pro Asp Ser Tyr Ser Trp Arg His Leu Pro Val Gly Lys Leu Glu
205                 210                 215                 220
tgaactaaac aatatccagg accacaacac catttgggaa ggctgctgca gactggagcc      1875
cacactgaag aatgcaagaa ttattggtga acgaactggc ttccggccag tacgccccca      1935
gattcggcta gaaagagaac agcttcgcac tggaccttca aacacagagg tcatccacaa      1995
ctatggccat ggaggctacg ggctcaccat ccactgggga tgtgccctgg aggcagccaa      2055
gctctttggg agaatcctgg aagaaagaa attgtccaga atgccaccat cccacctctg      2115
aagactccag tgactgctgc ctccccccac aagaactccc ttctcccctc agccaatgaa      2175
tcaatgtgct ccttcataag ccattgcttc tccctcactt ctttcctcaa agaagcatga      2235
ggtgagagaa agccacaaag tcagtgcctg gagaagggtt cagcccaaca tggggcccct      2295
ctcatcactg aaatccctct accttctctg ggtctggcat tataagaac agctgaggct      2355
gtcattccat gagtcttcag aagaaaggac agctcagaaa atcaaagagg ccaactgccc      2415
agagccacag aaaatggagg ataattgagg ctaagtaacc tgattacaag ttgtactaac      2475
atattaaagg ttctgaaaag tcctgcagca aagacaacta tctgatgttg tttaacccag      2535
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cttcccctca ggaaatagca tcctgtgtcc ccgcactgca gttgtctggt ctctccagca   120
gtttggtact tccggctgct gca atg cgt gtg gtg gtg att gga gca gga gtc   173
                          Met Arg Val Val Val Ile Gly Ala Gly Val
                           1   5   10

atc ggg ctg tcc acc gcc ctc tgc atc cat gag cgc tac cac tca gtc   221
Ile Gly Leu Ser Thr Ala Leu Cys Ile His Glu Arg Tyr His Ser Val
                15   20   25

ctg cag cca ctg gac ata aag gtc tac gcg gac cgc ttc acc cca ctc   269
Leu Gln Pro Leu Asp Ile Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu
            30   35   40

acc acc acc gac gtg gct gcc ggc ctc tgg cag ccc tac ctt tct gac   317
Thr Thr Thr Asp Val Ala Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp
        45   50   55

ccc aac aac cca cag gag gcg acc ctt cct gga agg aca cag ttc tgg   365
Pro Asn Asn Pro Gln Glu Ala Thr Leu Pro Gly Arg Thr Gln Phe Trp
    60   65   70

gat ttc gga agc tgacccccag agagctggat atgttcccag attacggcta   417
Asp Phe Gly Ser
75

tggctggttc cacacaagcc taattctgga gggaaagaac tatctacagt ggctgactga   477
aaggttaact gagagggggag tgaagttctt ccagcggaaa gtggagtctt ttgaggaggt   537
ggcaagagaa ggcgcagacg tgattgtcaa ctgcactggg gtatgggctg gggcgctaca   597
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aaacaatatc caggaccaca acaccatttg ggaaggctgc tgcagactgg agcccacact   837
gaagaatgca agaattattg gtgaacgaac tggcttccgg ccagtacgcc cccagattcg   897
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ccatgagtct tcagaagaaa ggacagctca gaaaatcaaa gaggccaact gcccagagcc   1377
acagaaaatg gaggataatt gaggctaagt aacctgatta caagttgtac taacatatta   1437
aaggttctga aaagtcctgc agcaaagaca actatctgat gttgtttaac ccagtgcttg   1497
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tcctccatgt tattcacagg gtctcagcac gattcatctc aaaggctgct gca atg      116
                                                              Met
                                                               1

cgt gtg gtg gtg att gga gca gga gtc atc ggg ctg tcc acc gcc ctc      164
Arg Val Val Val Ile Gly Ala Gly Val Ile Gly Leu Ser Thr Ala Leu
             5                  10                  15

tgc atc cat gag cgc tac cac tca gtc ctg cag cca ctg gac ata aag      212
Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile Lys
        20                  25                  30

gtc tac gcg gac cgc ttc acc cca ctc acc acc acc gac gtg gct gcc      260
Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala Ala
        35                  40                  45

ggc ctc tgg cag ccc tac ctt tct gac ccc aac aac cca cag gag gcg      308
Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu Ala
50                  55                  60                  65

gac tgg agc caa cag acc ttt gac tat ctc ctg agc cat gtc cat tct      356
Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His Ser
                70                  75                  80

ccc aac gct gaa aac ctg ggc ctg ttc cta atc tcg ggc tac aac ctc      404
Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn Leu
                85                  90                  95

ttc cat gaa gcc att ccg gtg gca aga gaa ggc gca gac gtg att gtc      452
Phe His Glu Ala Ile Pro Val Ala Arg Glu Gly Ala Asp Val Ile Val
            100                 105                 110

aac tgc act ggg gta tgg gct ggg gcg cta caa cga gac ccc ctg ctg      500
Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp Pro Leu Leu
        115                 120                 125

cag cca ggc cgg ggg cag atc atg aag gtg gac gcc cct tgg atg aag      548
Gln Pro Gly Arg Gly Gln Ile Met Lys Val Asp Ala Pro Trp Met Lys
130                 135                 140                 145

cac ttc att ctc acc cat gac cca gag aga ggc atc tac aat tcc ccg      596
His Phe Ile Leu Thr His Asp Pro Glu Arg Gly Ile Tyr Asn Ser Pro
                150                 155                 160

tac atc atc cca ggg acc cag aca gtt act ctt gga ggc atc ttc cag      644
Tyr Ile Ile Pro Gly Thr Gln Thr Val Thr Leu Gly Gly Ile Phe Gln
                165                 170                 175

ttg gga aac tgg agt gaa cta aac aat atc cag gac cac aac acc att      692
Leu Gly Asn Trp Ser Glu Leu Asn Asn Ile Gln Asp His Asn Thr Ile
            180                 185                 190

tgg gaa ggc tgc tgc aga ctg gag ccc aca ctg aag aat gca aga att      740
Trp Glu Gly Cys Cys Arg Leu Glu Pro Thr Leu Lys Asn Ala Arg Ile
        195                 200                 205

att ggt gaa cga act ggc ttc cgg cca gta cgc ccc cag att cgg cta      788
Ile Gly Glu Arg Thr Gly Phe Arg Pro Val Arg Pro Gln Ile Arg Leu
210                 215                 220                 225

gaa aga gaa cag ctt cgc act gga cct tca aac aca gag gtc atc cac      836
Glu Arg Glu Gln Leu Arg Thr Gly Pro Ser Asn Thr Glu Val Ile His
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                 230                    235                    240
aac tat ggc cat gga ggc tac ggg ctc acc atc cac tgg gga tgt gcc     884
Asn Tyr Gly His Gly Gly Tyr Gly Leu Thr Ile His Trp Gly Cys Ala
             245                    250                    255
ctg gag gca gcc aag ctc ttt ggg aga atc ctg gaa gaa aag aaa ttg     932
Leu Glu Ala Ala Lys Leu Phe Gly Arg Ile Leu Glu Glu Lys Lys Leu
             260                    265                    270
tcc aga atg cca cca tcc cac ctc tgaagactcc agtgactgct gcctcccccc    986
Ser Arg Met Pro Pro Ser His Leu
             275                    280

acaagaactc ccttctcccc tcagccaatg aatcaatgtg ctccttcata agccattgct   1046
tctccctcac ttctttcctc aaagaagcat gaggtgagag aaagccacaa agtcagtgcc   1106
tggagaaggg ttcagcccaa catggggccc ctctcatcac tgaaatccct ctaccttctc   1166
tgggtctggc attataaaga acagctgagg ctgtcattcc atgagtcttc agaagaaagg   1226
acagctcaga aaatcaaaga ggccaactgc ccagagccac agaaatgga ggataattga     1286
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Leu Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile
             20                  25                  30
Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala
             35                  40                  45
Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu
         50                  55                  60
Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His
65                  70                  75                  80
Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn
                 85                  90                  95
Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp Lys Asp Thr Val Leu
             100                 105                 110
Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp Met Phe Pro Asp Tyr
             115                 120                 125
Gly Tyr Gly Trp Phe His Thr Ser Leu Ile Leu Glu Gly Lys Asn Tyr
             130                 135                 140
Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg Gly Val Lys Phe Phe
145                 150                 155                 160
Gln Arg Lys Val Glu Ser Phe Glu Glu Val Ala Arg Glu Gly Ala Asp
                 165                 170                 175
Val Ile Val Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp
                 180                 185                 190
Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile Met Lys Val Asp Ala Pro
             195                 200                 205
Trp Met Lys His Phe Ile Leu Thr His Asp Pro Glu Arg Gly Ile Tyr
             210                 215                 220
Asn Ser Pro Tyr Ile Ile Pro Gly Thr Gln Thr Val Thr Leu Gly Gly
225                 230                 235                 240
Ile Phe Gln Leu Gly Asn Trp Ser Glu Leu Asn Asn Ile Gln Asp His
             245                 250                 255
Asn Thr Ile Trp Glu Gly Cys Cys Arg Leu Glu Pro Thr Leu Lys Asn
             260                 265                 270
Ala Arg Ile Ile Gly Glu Arg Thr Gly Phe Arg Pro Val Arg Pro Gln
             275                 280                 285
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Ile Arg Leu Glu Arg Glu Gln Leu Arg Thr Gly Pro Ser Asn Thr Glu
    290   295   300
Val Ile His Asn Tyr Gly His Gly Gly Tyr Gly Leu Thr Ile His Trp
305   310   315   320
Gly Cys Ala Leu Glu Ala Ala Lys Leu Phe Gly Arg Ile Leu Glu Glu
                325   330   335
Lys Lys Leu Ser Arg Met Pro Pro Ser His Leu
                340   345

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<213> Homo sapiens

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                20   25   30
Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala
        35   40   45
Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu
        50   55   60
Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His
65   70   75   80
Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn
                85   90   95
Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp Lys Asp Thr Val Leu
                100   105   110
Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp Met Phe Pro Asp Tyr
                115   120   125
Gly Tyr Gly Trp Phe His Thr Ser Leu Ile Leu Glu Gly Lys Asn Tyr
                130   135   140
Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg Gly Val Lys Phe Phe
145   150   155   160
Gln Arg Lys Val Glu Ser Phe Glu Glu Val Ala Arg Glu Gly Ala Asp
                165   170   175
Val Ile Val Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp
                180   185   190
Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile Met Lys Asp Pro Asp Ser
                195   200   205
Tyr Ser Trp Arg His Leu Pro Val Gly Lys Leu Glu
        210   215   220

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Leu Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile
                20   25   30
Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala
        35   40   45
Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu
        50   55   60
Ala Thr Leu Pro Gly Arg Thr Gln Phe Trp Asp Phe Gly Ser

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Leu Cys Ile His Glu Arg Tyr His Ser Val Leu Gln Pro Leu Asp Ile
            20   25   30
Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr Thr Thr Asp Val Ala
        35   40   45
Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro Asn Asn Pro Gln Glu
        50   55   60
Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu Leu Ser His Val His
65   70   75   80
Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu Ile Ser Gly Tyr Asn
                85   90   95
Leu Phe His Glu Ala Ile Pro Val Ala Arg Glu Gly Ala Asp Val Ile
                100   105   110
Val Asn Cys Thr Gly Val Trp Ala Gly Ala Leu Gln Arg Asp Pro Leu
        115   120   125
Leu Gln Pro Gly Arg Gly Gln Ile Met Lys Val Asp Ala Pro Trp Met
        130   135   140
Lys His Phe Ile Leu Thr His Asp Pro Glu Arg Gly Ile Tyr Asn Ser
145   150   155   160
Pro Tyr Ile Ile Pro Gly Thr Gln Thr Val Thr Leu Gly Gly Ile Phe
                165   170   175
Gln Leu Gly Asn Trp Ser Glu Leu Asn Asn Ile Gln Asp His Asn Thr
                180   185   190
Ile Trp Glu Gly Cys Cys Arg Leu Glu Pro Thr Leu Lys Asn Ala Arg
                195   200   205
Ile Ile Gly Glu Arg Thr Gly Phe Arg Pro Val Arg Pro Gln Ile Arg
        210   215   220
Leu Glu Arg Glu Gln Leu Arg Thr Gly Pro Ser Asn Thr Glu Val Ile
225   230   235   240
His Asn Tyr Gly His Gly Gly Tyr Gly Leu Thr Ile His Trp Gly Cys
                245   250   255
Ala Leu Glu Ala Ala Lys Leu Phe Gly Arg Ile Leu Glu Glu Lys Lys
                260   265   270
Leu Ser Arg Met Pro Pro Ser His Leu
        275   280

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<220>
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<222> 152
<223> 99-16105-152 : polymorphic base A or G

<220>
<221> misc_binding
<222> 140..164
<223> 99-16105-152.probe

<210>
<211> primer_bind
<212> 133..151
<213> 99-16105-152.mis

<220>
<221> primer_bind
<222> 153..171
<223> 99-16105-152.mis complement

<210>
<221> primer_bind
<222> 1..19
<223> 99-16105.pu

<220>
<221> primer_bind
<222> 437..456
<223> 99-16105.rp complement

<400> 11
cgctttgttg tattctttgt tatttatcca ttttgccaaa ttatctgcaa gtagaaatat   60
cgaaataaga agctctttag caatttactt tggatattgg ttttcttttg aaggacagtt   120
attaaaatag cttgtaggat tactcatttt crtttttctt cttttaaat ataaagcaat   180
gtcatcactt ttttccctgt attatatttc tcctcaataa ttgatatgct acattaaagg   240
aacacaaaat ggtcttaatt atgcaataat gatcaaggca aagagtgttt cctgggaact   300
aatggttgcc tgagaggagg tgatggcttg aggtccagct ggttattaag ccgcaggaaa   360
tgctgcaggc caagatttgt attatttctc tgagatgaaa atgaacccaa aaaaaggcaa   420
aatgggtttt tctccactaa tgggtaaaat gaactc   456

<210> 12
<211> 463
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 215
<223> 99-5919-215 : polymorphic base A or G

<220>
<221> misc_binding
<222> 203..227
<223> 99-5919-215.probe

<220>
<221> primer_bind
<222> 196..214
<223> 99-5919-215.mis

<220>
<221> primer_bind
<222> 216..234
<223> 99-5919-215.mis complement

<220>
<221> primer_bind
<222> 11..29

<223> 99-5919.pu

<210>
<211> primer_bind
<222> 445..465
<223> 99-5919.rp complement

<400> 13
ttttcttga ctacagcaat gcagatttca attctgccat tgaattccca gacatattcg   60
tttcccat tttcatcccc caccaccctg ccatttcctt cgtgttaact tgttttcctg   120
acttacagaa atcacctttt cctgtataca tttttaggat gtcagacttt attctaatga   180
ttttctcctag ttgcccccca aaattgtatt ctacrgtgtg attttaaagc tgaattttca   240
agttgatatt tcatatctat attttcacaa gctttcttc tatgaatgtt attgtcagct   300
gtcagggtgt gagatggtac ttgatactac attctttcca agctgttgcc tgaatcggtt   360
taaaacaaag tcattactag gctgtaaact gttgctctgc aaaattgagc agcacgtatt   420
taaccactca tacttcttag ctctccaaca ctttgagtcr ata   463

<210> 13
<211> 742
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..46

<220>
<221> CDS
<222> 47..508

<220>
<221> 3'UTR
<222> 509..742

<220>
<221> polyA_signal
<222> 718..723

<220>
<221> allele
<222> 21
<223> 8-135-112 : polymorphic base C or T

<220>
<221> allele
<222> 75
<223> 8-135-166 : polymorphic base A or C

<220>
<221> allele
<222> 135
<223> 99-16038-118 : polymorphic base A or G

<220>
<221> allele
<222> 194
<223> 8-137-152 : polymorphic base G or T

<220>

<221> allele
<222> 224
<223> 8-137-182   : polymorphic base A or G

<210>
<221> allele
<222> 390
<223> 8-130-220   : polymorphic base A or C

<210>
<221> allele
<222> 406
<223> 8-130-236   : polymorphic base A or G

<210>
<221> allele
<222> 573
<223> 8-131-199   : polymorphic base A or C

<210>
<221> allele
<222> 641
<223> 8-132-97   : polymorphic base C or T

<210>
<221> allele
<222> 708
<223> 8-132-164   : polymorphic base C or T

<210>
<221> allele
<222> 723
<223> 8-132-179   : polymorphic base A or T

<220>
<221> VARIANT
<222> 75
<223> Xaa=Ser or Tyr

<220>
<221> VARIANT
<222> 135
<223> Xaa=Lys or Arg

<220>
<221> VARIANT
<222> 194
<223> Xaa=Glu or Stop

<220>
<221> VARIANT
<222> 224
<223> Xaa=Gly or Arg

<220>
<221> VARIANT
<222> 390
<223> Xaa=Ala or Asp

<400> 13

tcatctctgc ttcacaatgc ygatgattta gctggagga cccaaa atg ctg gaa   55
                                                     Met Leu Glu
                                                      1

aag ctg atg ggt gct gat tmt ctc cag ctt ttc aga tcc aga tat aca   103
Lys Leu Met Gly Ala Asp Xaa Leu Gln Leu Phe Arg Ser Arg Tyr Thr
        5   10   15

ttg ggt aaa atc tac ttc ata ggt ttt caa arg agc att ctt ctg agc   151
Leu Gly Lys Ile Tyr Phe Ile Gly Phe Gln Xaa Ser Ile Leu Leu Ser
20   25   30   35

aaa tct gaa aac tct cta aac tct att gca aag gag aca gaa kaa gga   199
Lys Ser Glu Asn Ser Leu Asn Ser Ile Ala Lys Glu Thr Glu Xaa Gly
                40   45   50

aga gag acg gta aca agg aaa gaa rga tgg aag aga agg cat gag gac   247
Arg Glu Thr Val Thr Arg Lys Glu Xaa Trp Lys Arg Arg His Glu Asp
                55   60   65

ggc tat ttg gaa atg gca cag agg cat tta cag aga tca tta tgt cct   295
Gly Tyr Leu Glu Met Ala Gln Arg His Leu Gln Arg Ser Leu Cys Pro
            70   75   80

tgg gtc tct tac ctt cct cag ccc tat gca gag ctt gaa gaa gta agc   343
Trp Val Ser Tyr Leu Pro Gln Pro Tyr Ala Glu Leu Glu Glu Val Ser
        85   90   95

agc cat gtt gga aaa gtc ttc atg gca aga aac tat gag ttc ctt gmc   391
Ser His Val Gly Lys Val Phe Met Ala Arg Asn Tyr Glu Phe Leu Xaa
100   105   110   115

tat gag gcc tct aar gac cgc agg cag cct cta gaa cga atg tgg acc   439
Tyr Glu Ala Ser Lys Asp Arg Arg Gln Pro Leu Glu Arg Met Trp Thr
                120   125   130

tgc aac tac aac cag caa aaa gac cag tca tgc aac cac aag gaa ata   487
Cys Asn Tyr Asn Gln Gln Lys Asp Gln Ser Cys Asn His Lys Glu Ile
                135   140   145

act tct acc aaa gct gaa tgagtttgga agcagattct cccagccaa   535
Thr Ser Thr Lys Ala Glu
                150

tccttctgat gacaatgtag tctggccaac atcttcactg gamctgacg gactctgtgt   595
ctgggaccca gctgataaca cgtggtgatg ggattgtatt tgcaaytctc tggtcagtaa   655
gtgataaaat gccatttcta tgcacccacc tggcctgtgt gactgggaga atytctcttt   715
ttattaawtg tgcttcaagt tttaaca   742

<210> 14
<211> 153
<212> PRT
<213> Homo sapiens

<220>
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<222> 10
<223> Xaa=Ser or Tyr

<220>
<221> VARIANT
<222> 30
<223> Xaa=Lys or Arg

<220>
<221> VARIANT
<222> 50
<223> Xaa=Glu or Stop

43

<210>
<211> VARIANT
<212> 60
<223> Xaa=Gly or Arg

<210>
<211> VARIANT
<212> 115
<223> Xaa=Ala or Asp

<210>
<211> SITE
<222> 63..64
<223> basic protease cleavage site

<210>
<211> SITE
<222> 122..123
<223> basic protease cleavage site

<210>
<211> DISULFID
<222> 132..142

<210>
<211> PEPTIDE
<222> 1..64

<210>
<211> PEPTIDE
<222> 65..123

<210>
<211> PEPTIDE
<222> 124..153

<400> 14
Met Leu Glu Lys Leu Met Gly Ala Asp Xaa Leu Gln Leu Phe Arg Ser
1   5   10   15
Arg Tyr Thr Leu Gly Lys Ile Tyr Phe Ile Gly Phe Gln Xaa Ser Ile
            20   25   30
Leu Leu Ser Lys Ser Glu Asn Ser Leu Asn Ser Ile Ala Lys Glu Thr
            35   40   45
Glu Xaa Gly Arg Glu Thr Val Thr Arg Lys Glu Xaa Trp Lys Arg Arg
    50   55   60
His Glu Asp Gly Tyr Leu Glu Met Ala Gln Arg His Leu Gln Arg Ser
65   70   75   80
Leu Cys Pro Trp Val Ser Tyr Leu Pro Gln Pro Tyr Ala Glu Leu Glu
                85   90   95
Glu Val Ser Ser His Val Gly Lys Val Phe Met Ala Arg Asn Tyr Glu
                100   105   110
Phe Leu Xaa Tyr Glu Ala Ser Lys Asp Arg Arg Gln Pro Leu Glu Arg
            115   120   125
Met Trp Thr Cys Asn Tyr Asn Gln Gln Lys Asp Gln Ser Cys Asn His
    130   135   140
Lys Glu Ile Thr Ser Thr Lys Ala Glu
145   150

<210> 15

<210> 476
<212> DNA
<213> Homo sapiens

<400> 15
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cat gag gac ggc tat ttg gaa atg gca cag agg cat tta cag aga tca        48
His Glu Asp Gly Tyr Leu Glu Met Ala Gln Arg His Leu Gln Arg Ser
1               5                   10                  15
tta tgt cct tgg gtc tct tac ctt cct cag ccc tat gca gag ctt gaa        96
Leu Cys Pro Trp Val Ser Tyr Leu Pro Gln Pro Tyr Ala Glu Leu Glu
                20                  25                  30
gaa gta agc agc cat gtt gga aaa gtc ttc atg gca aga aac tat gag       144
Glu Val Ser Ser His Val Gly Lys Val Phe Met Ala Arg Asn Tyr Glu
        35                  40                  45
ttc ctt gcc tat gag gcc tct aag gac cgc agg cag cct cta gaa cga       192
Phe Leu Ala Tyr Glu Ala Ser Lys Asp Arg Arg Gln Pro Leu Glu Arg
        50                  55                  60
atg tgg acc tgc aac tac aac cag caa aaa gac cag tca tgc aac cac       240
Met Trp Thr Cys Asn Tyr Asn Gln Gln Lys Asp Gln Ser Cys Asn His
65                  70                  75                  80
aag gaa ata act tct acc aaa gct gaa tgagtttgga agcagattct             287
Lys Glu Ile Thr Ser Thr Lys Ala Glu
                85
tccagccaa tccttctgat gacaatgtag tctggccaac atcttcactg gactctgacg       347
gactctgtgt ctgggaccca gctgataaca cgtggtgatg ggattgtatt tgcaactctc       407
tggtcagtaa gtgataaaat gccatttcta tgcaccacc tggcctgtgt gactgggaga       467
atctctctt                                                              476
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<210> 16
<211> 89
<212> PRT
<213> Homo sapiens

<400> 16
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His Glu Asp Gly Tyr Leu Glu Met Ala Gln Arg His Leu Gln Arg Ser
1               5                   10                  15
Leu Cys Pro Trp Val Ser Tyr Leu Pro Gln Pro Tyr Ala Glu Leu Glu
                20                  25                  30
Glu Val Ser Ser His Val Gly Lys Val Phe Met Ala Arg Asn Tyr Glu
        35                  40                  45
Phe Leu Ala Tyr Glu Ala Ser Lys Asp Arg Arg Gln Pro Leu Glu Arg
        50                  55                  60
Met Trp Thr Cys Asn Tyr Asn Gln Gln Lys Asp Gln Ser Cys Asn His
65                  70                  75                  80
Lys Glu Ile Thr Ser Thr Lys Ala Glu
                85
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<210> 17
<211> 1533
<212> DNA
<213> Homo sapiens

<400> 17
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ttggggtcca ttgcaacccg aggcgagact agagttccca agcgagaagg gaagaggcag        60
tgggtgcacg tggaaggcgg acagaggct ggaaacaaga cgctccagaa tcaggagctt       120
cccctcagga aatagcatcc tgtgtccccg cactgcagtt gtctggtctc tccagcagtt       180
tggtacttcc ggctgctgca atg cgt gtg gtg gtg att gga gca gga gtc atc       233
                         Met Arg Val Val Val Ile Gly Ala Gly Val Ile
                         1               5                   10
```

```
ggg ctg tcc acc gcc ctc tgc atc cat gag cgc tac cac tca gtc ctg      281
Gly Leu Ser Thr Ala Leu Cys Ile His Glu Arg Tyr His Ser Val Leu
        15                  20                  25

cag cca ctg cac ata aag gtc tac gcg gac cgc ttc acc cca ctc acc      329
Gln Pro Leu His Ile Lys Val Tyr Ala Asp Arg Phe Thr Pro Leu Thr
        30                  35                  40

acc acc gac gtg gct gcc ggc ctc tgg cag ccc ttc ctt tct gac ccc      377
Thr Thr Asp Val Ala Ala Gly Leu Trp Gln Pro Tyr Leu Ser Asp Pro
        45                  50                  55

aac aac cca cag gag gtg gac tgg agc caa cag acc ttt gac tat ctc      425
Asn Asn Pro Gln Glu Ala Asp Trp Ser Gln Gln Thr Phe Asp Tyr Leu
60                  65                  70                  75

ctg agc cat gtc cat tct ccc aac gct gaa aac ctg ggc ctg ttc cta      473
Leu Ser His Val His Ser Pro Asn Ala Glu Asn Leu Gly Leu Phe Leu
                80                  85                  90

atc tcg ggc tac aac ctc ttc cat gaa gcc att ccg gac cct tcc tgg      521
Ile Ser Gly Tyr Asn Leu Phe His Glu Ala Ile Pro Asp Pro Ser Trp
                95                  100                 105

aag gac aca gtt ctg gga ttt cgg aag ctg acc ccc aga gag ctg gat      569
Lys Asp Thr Val Leu Gly Phe Arg Lys Leu Thr Pro Arg Glu Leu Asp
                110                 115                 120

atg ttc cca gat tac ggc tat ggc tgg ttc cac aca agc cta att ctg      617
Met Phe Pro Asp Tyr Gly Tyr Gly Trp Phe His Thr Ser Leu Ile Leu
        125                 130                 135

gag gga aag aac tat cta cag tgg ctg act gaa agg tta act gag agg      665
Glu Gly Lys Asn Tyr Leu Gln Trp Leu Thr Glu Arg Leu Thr Glu Arg
140                 145                 150                 155

gga gtg aag ttc ttc cag cgg aaa gtg gag tct ttt gag gag gtg gca      713
Gly Val Lys Phe Phe Gln Arg Lys Val Glu Ser Phe Glu Glu Val Ala
                160                 165                 170

aga gaa ggc gca gac gtg att gtc aac tgc act ggg gta tgg gct ggg      761
Arg Glu Gly Ala Asp Val Ile Val Asn Cys Thr Gly Val Trp Ala Gly
                175                 180                 185

gcg cta caa cga gac ccc ctg ctg cag cca ggc cgg ggg cag atc atg      809
Ala Leu Gln Arg Asp Pro Leu Leu Gln Pro Gly Arg Gly Gln Ile Met
        190                 195                 200

aag gtg gac gcc cct tgg atg aag cac ttc att ctc acc cat gac cca      857
Lys Val Asp Ala Pro Trp Met Lys His Phe Ile Leu Thr His Asp Pro
        205                 210                 215

gag aga ggc atc tac aat tcc ccg tac atc atc cca ggg acc cag aca      905
Glu Arg Gly Ile Tyr Asn Ser Pro Tyr Ile Ile Pro Gly Thr Gln Thr
220                 225                 230                 235

gtt act ctt gga ggc atc ttc cag ttg gga aac tgg agt gaa cta aac      953
Val Thr Leu Gly Gly Ile Phe Gln Leu Gly Asn Trp Ser Glu Leu Asn
                240                 245                 250

aat atc cag gac cac aac acc att tgg gaa ggc tgc tgc aga ctg gag      1001
Asn Ile Gln Asp His Asn Thr Ile Trp Glu Gly Cys Cys Arg Leu Glu
                255                 260                 265

ccc aca ctg aag aat gca aga att att ggt gaa gca act ggc ttc cgg      1049
Pro Thr Leu Lys Asn Ala Arg Ile Ile Gly Glu Ala Thr Gly Phe Arg
                270                 275                 280

cca gta cgc ccc cag att cgg cta gaa aga gaa cag ctt cgc act gga      1097
Pro Val Arg Pro Gln Ile Arg Leu Glu Arg Glu Gln Leu Arg Thr Gly
        285                 290                 295

cct tca aac aca gag gtc atc cac aac tat ggc cat gga ggc tac ggg      1145
Pro Ser Asn Thr Glu Val Ile His Asn Tyr Gly His Gly Gly Tyr Gly
300                 305                 310                 315

ctc acc atc cac tgg gga tgt gcc ctg gag gca gcc aag ctc ttt ggg      1193
Leu Thr Ile His Trp Gly Cys Ala Leu Glu Ala Ala Lys Leu Phe Gly
```

47

```
                325                         330                       335
Lys Lys Leu Ser Arg Met Pro Pro Ser His Leu
            340                     345


<210> 19
<211> 1200
<212> DNA
<213> Homo sapiens


<400> 19
atg gac aca gca cgg att gca gtt gtc ggg gca ggt gtg gtg ggg ctc      48
Met Asp Thr Ala Arg Ile Ala Val Val Gly Ala Gly Val Val Gly Leu
1                   5                   10                  15
tcc acg gct gtg tgc atc tcc aaa ctg gtg ccc cga tgc tcc gtt acc      96
Ser Thr Ala Val Cys Ile Ser Lys Leu Val Pro Arg Cys Ser Val Thr
                20                  25                  30
atc att tca gac aag ttt act cca gat acc acc agt gat gtg gca gcc     144
Ile Ile Ser Asp Lys Phe Thr Pro Asp Thr Thr Ser Asp Val Ala Ala
            35                  40                  45
gga atg ctt att cct cac act tat cca gat aca ccc att cac acg cag     192
Gly Met Leu Ile Pro His Thr Tyr Pro Asp Thr Pro Ile His Thr Gln
        50                  55                  60
aag cag tgg ttc aga gaa acc ttt aat cac ctc ttt gca att gcc aat     240
Lys Gln Trp Phe Arg Glu Thr Phe Asn His Leu Phe Ala Ile Ala Asn
65                  70                  75                  80
tct gca gaa gct gga gat gct ggt gtt cat ttg gta tca ggt tgg cag     288
Ser Ala Glu Ala Gly Asp Ala Gly Val His Leu Val Ser Gly Trp Gln
                85                  90                  95
ata ttt cag agc act ccg act gaa gaa gtg cca ttc tgg gct gac gtg     336
Ile Phe Gln Ser Thr Pro Thr Glu Glu Val Pro Phe Trp Ala Asp Val
                100                 105                 110
gtt ctg gga ttt cga aag atg act gag gct gag ctg aag aaa ttc ccc     384
Val Leu Gly Phe Arg Lys Met Thr Glu Ala Glu Leu Lys Lys Phe Pro
            115                 120                 125
cag tat gtg ttt ggt cag gct ttt aca acc ctg aaa tgt gaa tgc cct     432
Gln Tyr Val Phe Gly Gln Ala Phe Thr Thr Leu Lys Cys Glu Cys Pro
        130                 135                 140
gcc tac ctc ccg tgg ttg gag aaa agg ata aag gga agt gga ggc tgg     480
Ala Tyr Leu Pro Trp Leu Glu Lys Arg Ile Lys Gly Ser Gly Gly Trp
145                 150                 155                 160
aca ctc act cgg cga ata gaa gac ctg tgg gaa ctt cat ccg tcc ttt     528
Thr Leu Thr Arg Arg Ile Glu Asp Leu Trp Glu Leu His Pro Ser Phe
                165                 170                 175
gac atc gtg gtc aac tgt tca ggc ctt gga agc aga cag ctt gca gga     576
Asp Ile Val Val Asn Cys Ser Gly Leu Gly Ser Arg Gln Leu Ala Gly
                180                 185                 190
gac tca aag att ttc cct gta agg ggc caa gtc ctc caa gtt cag gct     624
Asp Ser Lys Ile Phe Pro Val Arg Gly Gln Val Leu Gln Val Gln Ala
            195                 200                 205
ccc tgg gtg gag cat ttt atc cga gat ggc agt ggg ctg aca tat att     672
Pro Trp Val Glu His Phe Ile Arg Asp Gly Ser Gly Leu Thr Tyr Ile
        210                 215                 220
tat cct ggt aca tcc cat gta acc cta ggt gga act agg caa aaa ggg     720
Tyr Pro Gly Thr Ser His Val Thr Leu Gly Gly Thr Arg Gln Lys Gly
225                 230                 235                 240
gac tgg aat ctg tcc ccg gat gca gaa aat agc aga gag att ctt tcc     768
Asp Trp Asn Leu Ser Pro Asp Ala Glu Asn Ser Arg Glu Ile Leu Ser
                245                 250                 255
cga tgc tgt gct ctg gag ccc tcc ctc cac gga gcc tgc aac atc agg     816
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48

```
Arg Cys Cys Ala Leu Glu Pro Ser Leu His Gly Ala Cys Asn Ile Arg
        250                 265             270
gag aag gtg ggc ttg agg ccc tac agg cca ggc gtg cga ctg cag aca      864
Glu Lys Val Gly Leu Arg Pro Tyr Arg Pro Gly Val Arg Leu Gln Thr
        275                 280             285
gag ctc ctt gcg cga gat gga cag agg ctg cct gta gtc cac cac tat      912
Glu Leu Leu Ala Arg Asp Gly Gln Arg Leu Pro Val Val His His Tyr
    290                 295                 300
ggc cat ggg agt ggg ggc atc tca gtg cac tgg ggc act gct ctg gag      960
Gly His Gly Ser Gly Gly Ile Ser Val His Trp Gly Thr Ala Leu Glu
305                 310                 315                 320
gcc gcc agg ctg gtg agc gag tgt gtc cat gcc ctc agg acc ccc att     1008
Ala Ala Arg Leu Val Ser Glu Cys Val His Ala Leu Arg Thr Pro Ile
                325                 330                 335
ccc aag tca aac ctg tagatgacat aaaatgacag caaagagact gagagactgt     1063
Pro Lys Ser Asn Leu
                340
tgatcaaagc acagaacagg ttcaaataac ttttccactg catgaaagtt taattagaca   1123
tttctttgtt ttcaacatta gaagtggtgt aacatgtaag ctgagcacgg tagcatgcct   1183
atagtcccag ctacttg                                                  1200


<210> 20
<211> 1023
<212> DNA
<213> Homo sapiens


<400> 20
atg gac aca gca cgg att gca gtt gtc ggg gca ggt gtg gtg ggg ctc       48
Met Asp Thr Ala Arg Ile Ala Val Val Gly Ala Gly Val Val Gly Leu
1                 5                 10                  15
tcc acg gct gtg tgc atc tcc aaa ctg gtg ccc cga tgc tcc gtt acc       96
Ser Thr Ala Val Cys Ile Ser Lys Leu Val Pro Arg Cys Ser Val Thr
                20                  25                  30
atc att tca gac aag ttt act cca gat acc acc agt gat gtg gca gcc      144
Ile Ile Ser Asp Lys Phe Thr Pro Asp Thr Thr Ser Asp Val Ala Ala
        35                  40                  45
gga atg ctt att cct cac act tat cca gat aca ccc att cac acg cag      192
Gly Met Leu Ile Pro His Thr Tyr Pro Asp Thr Pro Ile His Thr Gln
        50                  55                  60
aag cag tgg ttc aga gaa acc ttt aat cac ctc ttt gca att gcc aat      240
Lys Gln Trp Phe Arg Glu Thr Phe Asn His Leu Phe Ala Ile Ala Asn
65                  70                  75                  80
tct gca gaa gct gga gat gct ggt gtt cat ttg gta tca ggg ata aag      288
Ser Ala Glu Ala Gly Asp Ala Gly Val His Leu Val Ser Gly Ile Lys
                85                  90                  95
gga agt gga ggc tgg aca ctc act cgg cga ata gaa gac ctg tgg gaa      336
Gly Ser Gly Gly Trp Thr Leu Thr Arg Arg Ile Glu Asp Leu Trp Glu
            100                 105                 110
ctt cat ccg tcc ttt gac atc gtg gtc aac tgt tca ggc ctt gga agc      384
Leu His Pro Ser Phe Asp Ile Val Val Asn Cys Ser Gly Leu Gly Ser
            115                 120                 125
aga cag ctt gca gga gac tca aag att ttc cct gta agg ggc caa gtc      432
Arg Gln Leu Ala Gly Asp Ser Lys Ile Phe Pro Val Arg Gly Gln Val
        130                 135                 140
ctc caa gtt cag gct ccc tgg gtg gag cat ttt atc cga gat ggc agt      480
Leu Gln Val Gln Ala Pro Trp Val Glu His Phe Ile Arg Asp Gly Ser
145                 150                 155                 160
ggg ctg aca tat att tat cct ggt aca tcc cat gta acc cta ggt gga      528
Gly Leu Thr Tyr Ile Tyr Pro Gly Thr Ser His Val Thr Leu Gly Gly
```

```
                    165                      170                      175
act agg caa aaa ggg gac tgg aat ctg tcc ccg gat gca gaa aat agc        576
Thr Arg Gln Lys Gly Asp Trp Asn Leu Ser Pro Asp Ala Glu Asn Ser
            180                      185                      190
aga gag att ctt tcc cga tgc tgt gct ctg gag ccc tcc ctc cac gga        624
Arg Glu Ile Leu Ser Arg Cys Cys Ala Leu Glu Pro Ser Leu His Gly
            195                      200                      205
gcc tgc aac atc agg gag aag gtg ggc ttg agg ccc tac agg cca ggc        672
Ala Cys Asn Ile Arg Glu Lys Val Gly Leu Arg Pro Tyr Arg Pro Gly
        210                      215                      220
gtg cga ctg cag aca gag ctc ctt gcg cga gat gga cag agg ctg cct        720
Val Arg Leu Gln Thr Glu Leu Leu Ala Arg Asp Gly Gln Arg Leu Pro
225                      230                      235                      240
gta gtc cac cac tat ggc cat ggg agt ggg ggc atc tca gtg cac tgg        768
Val Val His His Tyr Gly His Gly Ser Gly Gly Ile Ser Val His Trp
                    245                      250                      255
ggc act gct ctg gag gcc gcc agg ctg gtg agc gag tgt gtc cat gcc        816
Gly Thr Ala Leu Glu Ala Ala Arg Leu Val Ser Glu Cys Val His Ala
            260                      265                      270
ctc agg acc ccc att ccc aag tca aac ctg tagatgacat aaaatgacag          864
Leu Arg Thr Pro Ile Pro Lys Ser Asn Leu
            275                      280
caaagagact gagagactgt tgatcaaagc acagaacagg ttcaaataac ttttccactg      924
catgaaagtt taattagaca tttctttgtt ttcaacatta gaagtggtgt aacatgtaag      984
ctgagcacgg tagcatgcct atagtcccag ctacttg                              1023


<210> 21
<211> 341
<212> PRT
<213> Homo sapiens

<400> 21
Met Asp Thr Ala Arg Ile Ala Val Val Gly Ala Gly Val Val Gly Leu
1               5                   10                  15
Ser Thr Ala Val Cys Ile Ser Lys Leu Val Pro Arg Cys Ser Val Thr
            20                  25                  30
Ile Ile Ser Asp Lys Phe Thr Pro Asp Thr Thr Ser Asp Val Ala Ala
        35                  40                  45
Gly Met Leu Ile Pro His Thr Tyr Pro Asp Thr Pro Ile His Thr Gln
    50                  55                  60
Lys Gln Trp Phe Arg Glu Thr Phe Asn His Leu Phe Ala Ile Ala Asn
65                  70                  75                  80
Ser Ala Glu Ala Gly Asp Ala Gly Val His Leu Val Ser Gly Trp Gln
                85                  90                  95
Ile Phe Gln Ser Thr Pro Thr Glu Glu Val Pro Phe Trp Ala Asp Val
            100                 105                 110
Val Leu Gly Phe Arg Lys Met Thr Glu Ala Glu Leu Lys Lys Phe Pro
        115                 120                 125
Gln Tyr Val Phe Gly Gln Ala Phe Thr Thr Leu Lys Cys Glu Cys Pro
    130                 135                 140
Ala Tyr Leu Pro Trp Leu Glu Lys Arg Ile Lys Gly Ser Gly Gly Trp
145                 150                 155                 160
Thr Leu Thr Arg Arg Ile Glu Asp Leu Trp Glu Leu His Pro Ser Phe
                165                 170                 175
Asp Ile Val Val Asn Cys Ser Gly Leu Gly Ser Arg Gln Leu Ala Gly
            180                 185                 190
Asp Ser Lys Ile Phe Pro Val Arg Gly Gln Val Leu Gln Val Gln Ala
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Pro Trp Val Glu His Phe Ile Arg Asp Gly Ser Gly Leu Thr Tyr Ile
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Tyr Pro Gly Thr Ser His Val Thr Leu Gly Gly Thr Arg Gln Lys Gly
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Arg Cys Cys Ala Leu Glu Pro Ser Leu His Gly Ala Cys Asn Ile Arg
            260                      265                      270
Glu Lys Val Gly Leu Arg Pro Tyr Arg Pro Gly Val Arg Leu Gln Thr
            275                      280                      285
Glu Leu Leu Ala Arg Asp Gly Gln Arg Leu Pro Val Val His His Tyr
            290                      295                      300
Gly His Gly Ser Gly Gly Ile Ser Val His Trp Gly Thr Ala Leu Glu
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Pro Lys Ser Asn Leu
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Gly Met Leu Ile Pro His Thr Tyr Pro Asp Thr Pro Ile His Thr Gln
        50                      55                      60
Lys Gln Trp Phe Arg Glu Thr Phe Asn His Leu Phe Ala Ile Ala Asn
65                      70                      75                      80
Ser Ala Glu Ala Gly Asp Ala Gly Val His Leu Val Ser Gly Ile Lys
                    85                      90                      95
Gly Ser Gly Gly Trp Thr Leu Thr Arg Arg Ile Glu Asp Leu Trp Glu
                    100                     105                     110
Leu His Pro Ser Phe Asp Ile Val Val Asn Cys Ser Gly Leu Gly Ser
            115                     120                     125
Arg Gln Leu Ala Gly Asp Ser Lys Ile Phe Pro Val Arg Gly Gln Val
        130                     135                     140
Leu Gln Val Gln Ala Pro Trp Val Glu His Phe Ile Arg Asp Gly Ser
145                     150                     155                     160
Gly Leu Thr Tyr Ile Tyr Pro Gly Thr Ser His Val Thr Leu Gly Gly
                    165                     170                     175
Thr Arg Gln Lys Gly Asp Trp Asn Leu Ser Pro Asp Ala Glu Asn Ser
                    180                     185                     190
Arg Glu Ile Leu Ser Arg Cys Cys Ala Leu Glu Pro Ser Leu His Gly
            195                     200                     205
Ala Cys Asn Ile Arg Glu Lys Val Gly Leu Arg Pro Tyr Arg Pro Gly
        210                     215                     220
Val Arg Leu Gln Thr Glu Leu Leu Ala Arg Asp Gly Gln Arg Leu Pro
225                     230                     235                     240
Val Val His His Tyr Gly His Gly Ser Gly Gly Ile Ser Val His Trp
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Gly Thr Ala Leu Glu Ala Ala Arg Leu Val Ser Glu Cys Val His Ala
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